

METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND  
ASSESSMENT OF CANCER THERAPIES

Abstract of the Disclosure

- 5 The present invention is directed to the identification of markers that can be used to determine whether cancer cells are sensitive or resistant to a therapeutic agent. The present invention is also directed to the identification of therapeutic targets. Nucleic acid arrays were used to determine the level of expression of approximately 6500 nucleic acid sequences (genes) found in 54 different solid tumor cancer cell lines
- 10 selected from the NCI 60 cancer cell line series. After the level of expression was determined for each of the 6500 genes in each of the 54 cancer cell lines, statistical analysis was used to identify genes whose expression correlated with sensitivity or resistance to any one of 171 different anti-cancer compounds. Expression analysis was also used to identify genes associated with resistance or sensitivity to TAXOL in a
- 15 number of cancer cell lines, clinical samples, and a human mammary epithelial cell primary cell line. The invention features a number of "sensitivity genes." These are genes that are expressed in most or all cell lines that are sensitive to treatment with an agent and which are not expressed (or are expressed at a rather low level) in cells that are resistant to treatment with that agent. The invention also features a number of
- 20 "resistance genes." These are genes that are expressed in most or all cell lines that are resistant to treatment with an agent and which are not expressed (or are expressed at a rather low level) in cells that are sensitive to treatment with that agent.